

**AMENDMENTS TO THE SPECIFICATION**

Please replace the paragraph beginning on page 3, line 4 of the specification with the following paragraph:

As shown in panel [[B]]C, in healthy subjects carrying only the wild type sequence after digestion with TspR1 the amplified DNA of 421 base pairs is not cleaved. In the subjects affected by the disease heterozygous for the mutation, the amplified DNA is digested into a band of 421 base pairs (wild type allele) and two fragments of respectively 238 and 183 base pairs (the latter is not visible in Fig. 2b Figure 1C). (+/+): homozygous subjects for wild type ferroportin, (+/-): heterozygous subjects for the mutation.

Please replace the paragraph beginning on page 25, line 9 of the specification with the following paragraph:

The sequence of the full length cDNA coding for the mutated form of ferroportin at position 80 (G80S) is reported as ~~HDN3 sequence~~ SEQ ID NO:3 in the sequences listing annex.[[.]] Figure 1[[B]]C show the restriction pattern of the amplified genomic DNA of each individual: in the healthy subjects having only the wild type sequence, after digestion with Tspr1 the fragment of amplified DNA with the oligonucleotide pairs 13 ~~and~~ and 14, of 421 base pairs, is not cleaved.

Please replace the paragraph beginning on page 25, line 15 of the specification with the following paragraph:

In affected subjects, heterozygous for the mutation, the amplified DNA is cleaved into a band of 421 base pairs (wild type allele) and two bands of 238 and 183 base pairs (this last not visible in FIGURE 1b Figure 1C).